



**PSMA3 (NM\_002788.4) - cDNA + Protein - 2026-05-08**

ACTAGTTTGC GGCATCCTGT GGTATAGGGG AAGCGCTCCG GGCCTGGAAT -29

CCCTACGCGT CCCTTTGGGT TTAGCACGAT GAGCTCAATC GGCCTGGGT 22

Me tSerSerIle GlyThrGlyT 8

ATGACCTGTC AGCCTCTACA TTCTCTCCTG ACGGAAGAGT TTTTCAAGTT 72

yrAspLeuSe rAlaSerThr PheSerProA spGlyArgVa lPheGlnVal 24

GAATATGCTA TGAAGGCTGT GGAAAATAGT AGTACAGCTA TTGGAATCAG 122

GluTyrAlaM etLysAlaVa lGluAsnSer SerThrAlaI leGlyIleAr 41

ATGCAAAGAT GGTGTTGTCT TTGGGGTAGA AAAATTAGTC CTTTCTAAAC 172

gCysLysAsp GlyValValP heGlyValGl uLysLeuVal LeuSerLysL 58

TTTATGAAGA AGGTTCCAAC AAAAGACTTT TTAATGTTGA TCGGCATGTT 222

euTyrGluGl uGlySerAsn LysArgLeuP heAsnValAs pArgHisVal 74

GGAATGGCAG TAGCAGGTTT GTTGGCAGAT GCTCGTTCTT TAGCAGACAT 272

GlyMetAlaV aAlaGlyLe uLeuAlaAsp AlaArgSerL euAlaAspIl 91

AGCAAGAGAA GAAGCTTCCA ACTTCAGATC TAACTTTGGC TACAACATTC 322

eAlaArgGlu GluAlaSerA snPheArgSe rAsnPheGly TyrAsnIleP 108

CACTAAAACA TCTTGCAGAC AGAGTGGCCA TGTATGTGCA TGCATATACA 372

roLeuLysHi sLeuAlaAsp ArgValAlaM etTyrValHi sAlaTyrThr 124

CTCTACAGTG CTGTTAGACC TTTTGGCTGC AGTTTCATGT TAGGGTCTTA 422

LeuTyrSerA laValArgPr oPheGlyCys SerPheMetL euGlySerTy 141

CAGTGTGAAT GACGGTGCGC AACTCTACAT GATTGACCCA TCAGGTGTTT 472 [N144S](#) [A147T](#)

rSerValAsn AspGlyAlaG lnLeuTyrMe tIleAspPro SerGlyValS 158

CATACGGTTA TTGGGGCTGT GCCATCGGCA AAGCCAGGCA AGCTGCAAAG 522

erTyrGlyTy rTrpGlyCys AlaIleGlyL ysAlaArgGl nAlaAlaLys 174

ACGGAAATAG AGAAGCTTCA GATGAAAGAA ATGACCTGCC GTGATATCGT 572

ThrGluIleG luLysLeuGl nMetLysGlu MetThrCysA rgAspIleVa 191

TAAAGAAGTT GCAAAAATAA TTTACATAGT ACATGACGAA GTTAAGGATA 622 [Y199C](#)

lLysGluVal AlaLysIleI leTyrIleVa lHisAspGlu ValLysAspL 208

AAGCTTTTGA ACTAGAACTC AGCTGGGTTG GTGAATTAAC TAATGGAAGA 672

ysAlaPheGl uLeuGluLeu SerTrpValG lyGluLeuTh rAsnGlyArg 224

CATGAAATTG TTCCAAAAGA TATAAGAGAA GAAGCAGAGA AATATGCTAA 722 [p.R233del](#)

HisGluIleV alProLysAs pIleArgGlu GluAlaGluL ysTyrAlaLy 241

GGAATCTCTG AAGGAAGAAG ATGAATCAGA TGATGATAAT ATGTAACATT \*4

sGluSerLeu LysGluGluA spGluSerAs pAspAspAsn MetStop

TACTCCAGCA TCTATTGTAT TTTAAATTC TACTCCAGTC CAATGTAAC \*54

ATTAGCCCT GGATTATACA TACTGTCAA TTTTCATTAA ATTTTGTCT \*104

TATAA

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